



Universidad
Carlos III de Madrid



This is a postprint version of the following published document:

González Rodríguez, D., Hernández Carrión, J.R.(2015).
Decentralization and Heterogeneity in complex adaptative
systems. *Kybernetes*, Vol.44, Issue 6/7, pp.1082-1093.
Available in: <http://dx.doi.org/10.1108/K-01-2015-0030>

© Emerald Group

Decentralization and heterogeneity in complex adaptive systems

Diego Gonzalez-Rodriguez and Jose Rodolfo Hernandez-Carrion
Group of Economics and Complexity, University of Valencia, Valencia, Spain

Abstract. Following a bacterial-based modeling approach, the authors want to model and analyze the impact of both decentralization and heterogeneity on group behavior and collective learning. The paper aims to discuss these issues. Inspired by bacterial conjugation, the authors have defined an artificial society in which agents' strategies adapt to changes in resources location, allowing migration, and survival in a dynamic sugarscape-like scenario. To study the impact of these variables the authors have simulated a scenario in which resources are limited and localized. The authors also have defined three constraints in genetic information processing (inhibition of plasmid conjugation, inhibition of plasmid reproduction and inhibition of plasmid mutation). The results affirmed the hypothesis that efficiency of group adaptation to dynamic environments is better when societies are varied and distributed than when they are homogeneous and centralized. The authors have demonstrated that in a model based on free interactions among autonomous agents, optimal results emerge by incrementing heterogeneity levels and decentralization of communication structures, leading to a global adaptation of the system. This organic approach to model peer-to-peer dynamics in complex adaptive systems (CAS) is what the authors have named "bacterial-based algorithms" because agents exchange strategic information in the same way that bacteria use conjugation and share genome.

Keywords: Information theory, Adaptation, Emergence, Autopoiesis, Social systems, Intelligent agents

Paper type: Research paper

1. Introduction

In this paper we shall introduce an agent-based approach inspired by bacterial conjugation to model resilience in artificial societies. Even though similar approaches have been previously reported, such as OBBC (Muller *et al.*, 2002) or BEA (Nemiche *et al.*, 2013), we have developed a proof-of-concept inspired by bacterial conjugation that allows us to show how, in artificial societies based on interactions between agents with bounded rationality, better results emerge by incrementing heterogeneity levels and decentralization of communication structures (Heylighen, 1999). We consider bounded rationality in the sense of Simon (1991), i.e., the rationality of social agents, as a solution-search-oriented process, is limited by information in a cognitive sense. Therefore, decisions are constraint by information access and information processing. The paper also builds on the concept of bacterial-based algorithms as it was developed by Gonzalez-Rodriguez and Hernandez-Carrion (2014).

Bacterial conjugation is a distributed communication system used by bacteria to exchange strategies of survival implemented on genetic code (Thomas and Nielsen, 2005; Davison, 1999). It matches the kind of dynamics we want to model because of several reasons. First of all, we conceive both natural and artificial societies as CAS (Lansing, 2003) which evolution depends on the interactions of autonomous agents. Second, we sustain that

collective adaptation is related to decentralized communications (Baran, 1964; Givigi and Schwartz, 2014), with information exchanges by using peer-to-peer (P2P) networks to share codified blocks of information. Third, because even though communication and P2P dynamics play an important role, also heterogeneity in population, and variation of strategies are factors of evolution. These issues can be considered to develop new technical approaches, not only in bio-inspired mobile robotics (Nurzaman *et al.*, 2012) but also in systems oriented to swarm intelligence (Pini *et al.*, 2013).

In this paper we show how decentralization and heterogeneity play an important role on group adaptation, above all in dynamic environments with unpredictable changes. We have modeled an artificial society by using our bacterial-based approach in order to study how agents' strategies adapt to changes in resource location, allowing migration, and survival in dynamic "sugarscape-like" scenarios (Duffy *et al.*, 1998).

2. Description of the model

2.1 Agents

Following a bacterial-based modeling approach, we want to simulate and analyze the impact of both decentralization and heterogeneity on group adaptation. Our approach is inspired by bacterial conjugation and may be classified under the methodological paradigm of agent-based modeling. In agent-based modeling (Izquierdo *et al.*, 2008), agents with bounded rationality interact in a common environment, guided by local rules, leading to CAS that are named "artificial societies" (Duffy *et al.*, 1998; Nemiche *et al.*, 2013). These virtual representations of biological communities grow from the bottom up in computational environments and can be used as laboratories to test some hypotheses.

In this model, we have a set A with N agents (a_i). Each agent owns a genome (Mitchell, 1998) with a specific strategy (s_i) that determines its motor behavior. We conceive homeostasis as Cannon (1940) as the self-regulation of a system in order to keep the stability of its internal variables. In our model, homeostasis is related with agent behavior and metabolism. Agents try to survive by keeping their level of energy higher than E_{\min} by following their own genetic rules in order to find resources (Figure 1). We have fixed the value of E_{\min} at 1.89 k (energy units) and the initial energy of each agent at 197.5 k to normalize the behavior of the agents and track the evolution of the system with a single processor machine.

Agents with more successful genome will keep higher energy levels and will dominate the "cultural life" of society because the information of their genes will be propagated. Energy levels impact on:

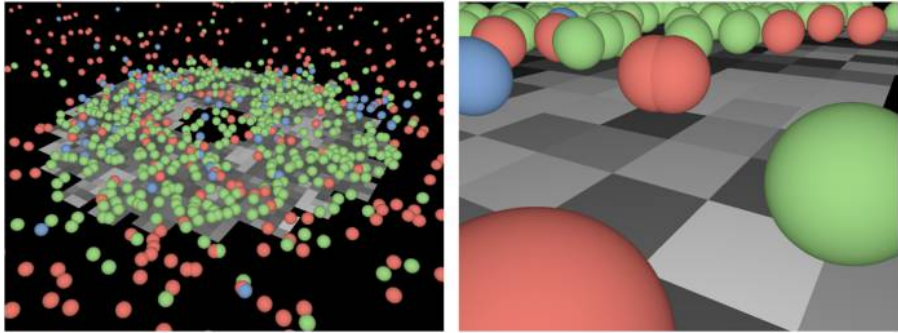
- (1) Vertical propagation of genetic information by reproduction.

Any iteration of simulation (t), agents consume energy as a consequence of their metabolism; the rate of energy consumption can be modified but we have fixed its value at 20 k/t for most of the simulations. Agents whose energy levels decrease, becoming lower than E_{\min} will eventually die. Agents with more energy than E_{\max} (215.48 k) are able to reproduce, yielding a new agent with similar genes that preserve successful strategies. Reproduction implies an energy cost (R_{cost}) initially fixed to 17.5 k according to our model normalization:

- (2) Horizontal propagation of genetic information by conjugation.

The success of genes will be evaluated in relation to the success of motor behavior in location of resources, i.e., agent skills to find resources and keep high energy levels.

Figure 1. Heterogeneous community of agents struggling for survival



Notes: Agents' colors depend on energy levels. Red means that agent's energy is lower than 107.74 k (50 percent of E_{\max}), green implies more than 150.84 k (70 percent of E_{\max}) and blue represents energy levels between both values. Black squares mean that at that location there are not resources. Gray squares vary their white component depending on resources available; the darker it is, the lower energy it offers. On the right, two agents with the same coordinates exchange a plasmid with genetic information

Then genome will affect agents' position in social structure. At each interaction (t), agents move randomly in the discrete space, following an Euclidean neighborhood model, i.e., with a probability space of four possible positions. In this shared medium, when two agents (a_a, a_b) have the same coordinates (x, y) they compare their energy levels. The agent with more energy (a_b) is allowed by default to propagate its genome horizontally by using conjugation. Otherwise, if conjugative machinery to send plasmids is inhibited in a_b , it does not share any genomic information and a_a does not "learn" any new strategy. In this case we will say that a_b configuration *inhibits plasmid conjugation*.

Even when the owner of a successful strategy (a_b) allows an agent with lower energy (a_a) to get a copy of that genome and then improve its strategy, a_b also can impose two restriction policies to that copy:

- (1) *Inhibit plasmid reproduction:* the receiver of a plasmid (a_a) is allowed to use the strategy that is contained in the copy but this copy cannot be sent to others once it is received. In this case the owner of the original plasmid (a_b) is the only one that can share his strategy.
- (2) *Inhibit plasmid mutation:* the receiver (a_a) can use the strategy but he cannot modify it. Genome only can be used as a unit of privative software or as a behavioral dogma, following the exact strategy proposed by the first owner (a_b). Otherwise, if mutation is not inhibited, strategies may be modified or mixed with other ones by the receiver (a_a) depending of two parameters: mutation rate (R_m) and recombination rate (R_R).

2.2 Agent genome

Agent genome is a data structure with 13 information blocks: three inhibitor genes with Boolean values (IGP, IGR, IGO) and ten strategic genes (SGA, SGB, SGC, SGD, SGE, SGF, SGG, SGH, SGI, SGJ) with real values between 0 and 360.

In our model, each agent (a_i) of the set A has its own strategy (s_i) coded as a part of its genome. This strategy is produced by the conjunction of strategic genes and motor actuators.

Considering a set “Str” containing several strategies (s_i), its cardinality $|\text{Str}|$ (number of different strategies in the population) will be equal or bigger than unity and equal or smaller than cardinality of A. We will denote it as:

$$\forall a_i \in A \exists s_i \in \text{Str} \quad (1)$$

$$1 \leq |\text{Str}| \leq |A|$$

If by default the value of $|\text{Str}|$ is one we will be starting our simulation in a completely homogeneous society. If this value is near to $|A|$ we will be analyzing a heterogeneous society. We will take the second option by default in our experiments.

Each agent has a genome with a segment containing one coded strategy ($\text{SGA}_i, \text{SGB}_i, \text{SGC}_i, \text{SGD}_i, \text{SGE}_i, \text{SGF}_i, \text{SGG}_i, \text{SGH}_i, \text{SGI}_i, \text{SGJ}_i$) of the set “Str.” But genome also contains three Boolean variables ($\text{IGP}, \text{IGR}, \text{IGO}$) whose positive activation will produce the expression of three inhibitors ($\text{P}, \text{R}, \text{O}$). These inhibitors are related with the three constraints explained above:

- (1) inhibit original plasmid conjugation (P);
- (2) inhibit plasmid copy reproduction (R); and
- (3) inhibit plasmid code mutation (O).

If there is P then the genome will not be released by conjugation, that is, that strategy will be private. So only the absence of P enables the first owner of the genome to act as a donor; that is, to send a copy of genome as a plasmid to another agent by using conjugation. If the possibility of P is high, then society will follow a centralized paradigm; that is, just some nodes will be able to send information. P implies that original genome will never be copied and sent to anybody else. Then, strategies of nodes without P and a successful strategy coded on S will dominate the culture.

If there is R this means that the receivers of a copy of a genome are not allowed to resend the replicated plasmid to another agent. It avoids decentralized propagation of strategies, considering that the original owners of a genome are the only ones that can distribute copies. High possibility of R implies a constraint to diffusion of received strategies, because the receiver will be able to use the successful strategy but will not be allowed to share that genetic information with others.

Decentralization is inversely related with these two parameters. High P and R rates imply centralized societies without P2P communication and without plasmid reproduction rights. Oppositely, low P and R rates lead to P2P exchanges of information without limits of copies.

During a conjugation process, when one agent sends a plasmid to another, the s_i sequence (which contains a copy of the strategy of the donor) could be modified. This means that mutation of any strategy is allowed by default. But mutation can be inhibited if O is present in the genome. O sequence implies that a plasmid cannot be modified. So only low levels of O presence lead to an open society in which variation of bad strategies in short time is guaranteed. However, high presence of O in the population genome implies that strategies are closed and invariant. So once an agent follows a specific strategy he cannot change it until he receives another genome from a more successful agent. Differentiation of strategies is another important variable in this model. Cardinality of “Str” is related with the number of different strategies by default, so if $|\text{Str}|$ is near to $|A|$ and there is a low presence of O segments in population genome then it implies more heterogeneity.

2.3 Resources

In order to study the impact of these three constraints (inhibition of plasmid conjugation, plasmid reproduction and plasmid mutation) in group adaptation to dynamic environments, we have designed a community of agents with $|\text{Str}| = |A|$.

We have supposed a scenario in which resources are limited and localized. Then, there are spatial locations where life is easier and places where survival is impossible without migration. Even though resources can be produced again after they have been eaten, the environment sustainability depends of the number of agents that consume them. That is, if there is a place rich in resources then agents with access to it will increase their energy, will reproduce and will produce a consumption overload (Figure 2). But once a threshold is achieved, some of them will die because there would be more consumption than production. That is, the chaotic dynamics will fall in an attractor that will define the state of balance of the ecosystem.

During the evolution of the system, agents with a close location to resources will appear, producing sedentary communities. There will also be communities of nomads (nomadic groups), that is, groups of agents that will move only periodically to areas with resources in order to increase their energy before exploring other regions.

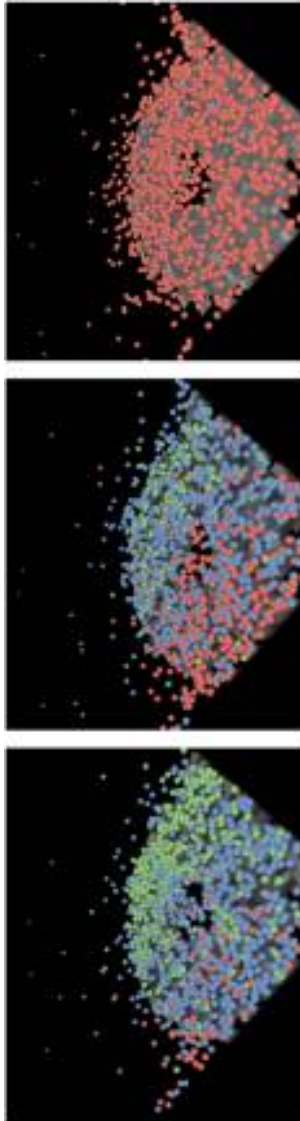
If the environment is static we can infer that being sedentary will be a good strategy once an agent arrives to an area with enough resources. We can think then that nomad behavior is useless, or even dangerous. In general, nomads have lower energy levels than sedentary agents because they spend more time distant than close to resources. In this sense, even though if one nomad eventually met a sedentary agent when it was visiting the rich area, the sedentary one will never copy its strategy after comparing both energy levels. If the environment is dynamic, however, nomad strategies are very useful for the species. If the location of resources changes drastically, only nomads will be able to achieve new resources, increasing their energy levels while sedentary levels decrease. In that case, some old sedentary communities will copy nomads' genomic strategies moving through new rich areas. Some of them will adapt to sedentary strategies again but in the new place (Figure 3).

3. Experimental results

Every initial configuration leads to a state of balance at one point of the simulation. However, the fitness of the system is greater if we remove some constraints, leading to a state of balance with a bigger population in the ecosystem. In that sense, we have studied how different configurations lead to different scenarios, and how in dynamic environments, fitness is improved with heterogeneous and decentralized societies. Furthermore, we have observed how intelligent behavior may emerge from social exchanges even when individual cognition is bounded.

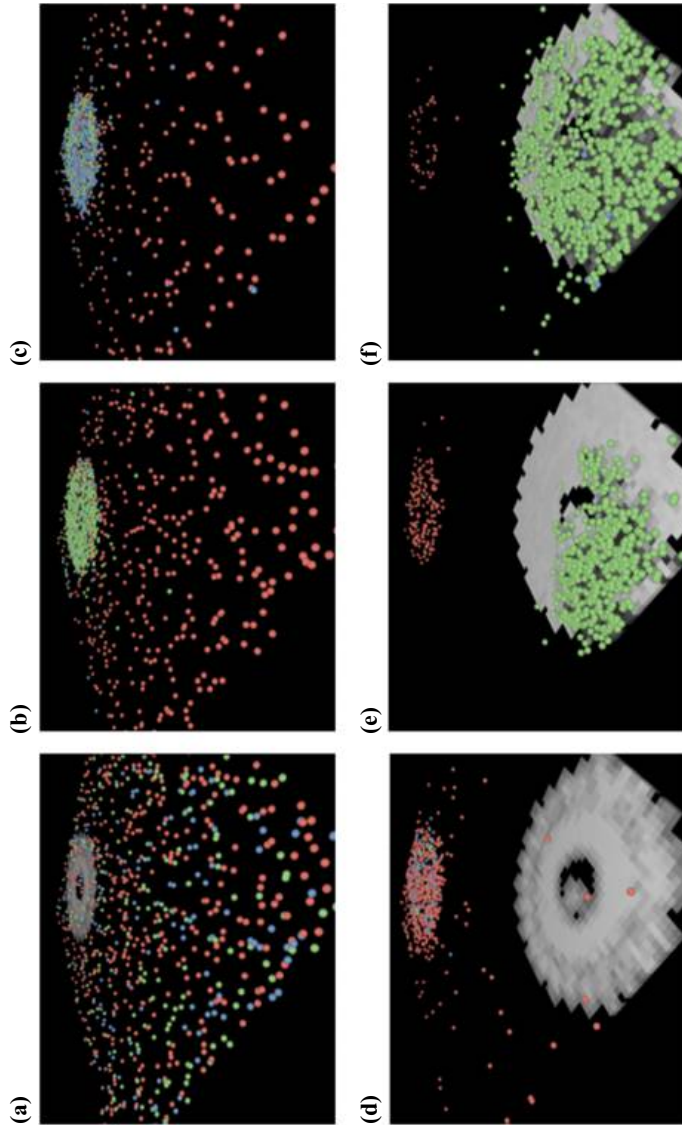
The focus of this study is to determine how probabilistic distribution of Boolean genes (P, R, O) affects social adaptation to dynamic environments with changes in resources location. We have fixed $|\text{Str}| \sim |A|$ and the recombination to 0.5, when mutation occurs. For any of those $|Z|^3$ setup configurations, we have executed our model for 5×10^3 iterations. Repeating each one of these experiments with random configurations and 10^3 agents as an initial population, we have observed common patterns that are related with P, R and O presence in population genome. We have tested the emergence of different global configurations and states of balance, concluding that both heterogeneity and decentralization are important to group adaptation and development. We have realized also that heterogeneity (Figures 4 and 5) has a small impact on global performance compared to decentralization (Figures 6 and 7). If we compare global results of

Figure 2. Consumption overload leading to a state of balance



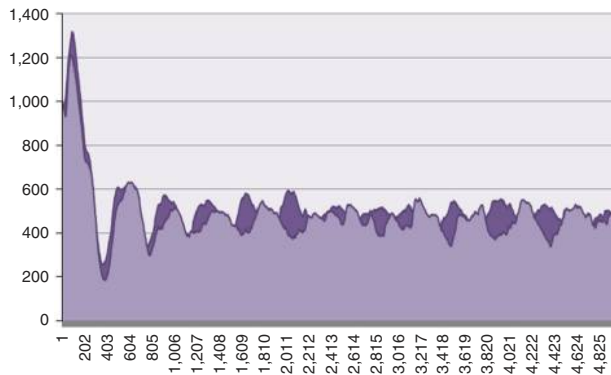
Notes: The system evolves from a society with high energy levels (green and blue) to one with lower consumption and less agents. A society with a low reproduction rate emerges and preservation of enough resources allows community to survive as a whole

Figure 3. Social dynamics in a changing environment

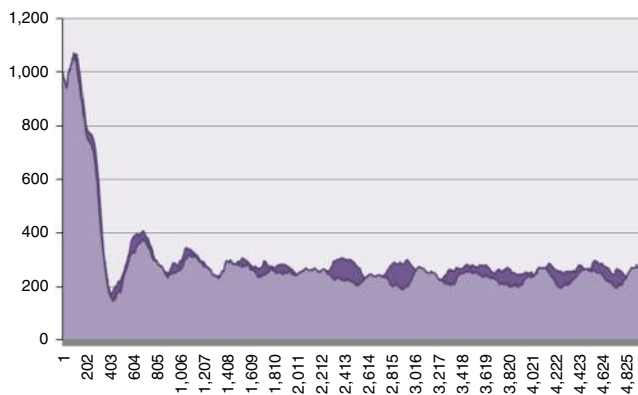


Notes: In the first snapshots (A, B, C) resources are located in the north, where most agents survive with sedentary strategies. When a resource location changes drastically (D) some agents remain with nomad strategies so some of them head to the south. Finally, the species is able to survive, leading to a new sedentary community in the south (E, F)

Figure 4. Population average in decentralized societies



Notes: Initial population: 10^3 agents. Iterations: $5 \times 10^3 t$.
 Repetitions: 10. When decentralization is forced, heterogeneous societies (dark) have a concentrated but higher population average than homogenous ones (light)

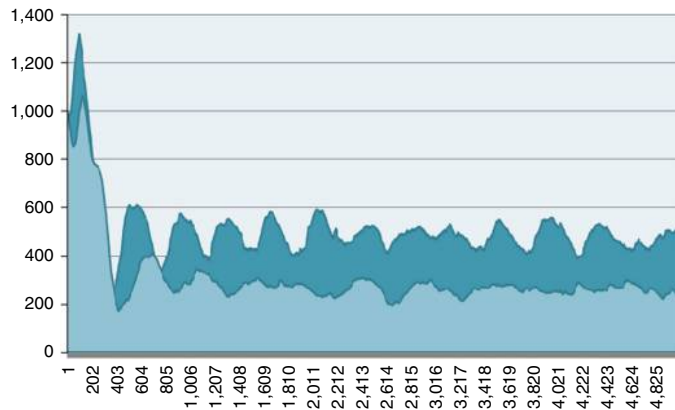


Notes: Initial population: 10^3 agents. Iterations: $5 \times 10^3 t$.
 Repetitions: 10. When centralization is forced, heterogeneous societies (dark) have a concentrated but higher population average than homogenous ones (light)

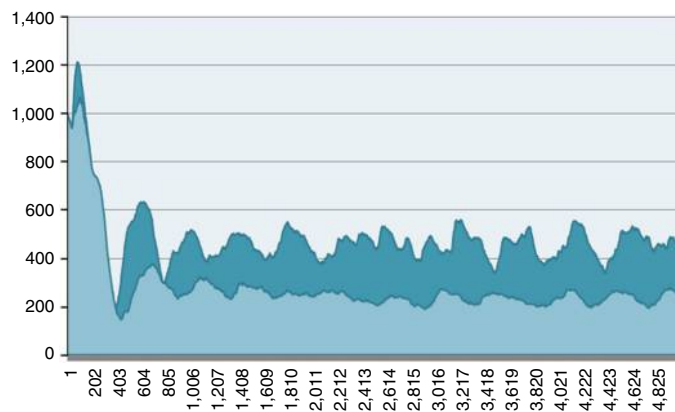
Figure 5. Population average in centralized societies

homogeneous societies (average: 384, max: 1,130, min: 190) with heterogeneous ones (average: 407, max: 1,161, min: 244), the latter are fitter for survival. Maximum differences are depreciable because they are achieved during the consumption overload phase, but difference in minimum is something to consider, because it can lead to population extinction as it happened in one experiment with a homogeneous society. If we compare centralized societies (average: 296, max: 1,055, min: 164) and decentralized ones (average: 495, max: 1,261, min: 223) the difference is notable. P and R absence in population genome implies a huge improvement in the fitness of population, showing the impact of decentralization on group adaptation to dynamic environments. We have used Netlogo 5.0.4 (Lytinen and Railsback, 2012; Netlogo, 2009; Robertson, 2005) the Raytracing extension (Stonedahl and Duan, 2011) to implement and visualize our model.

Figure 6. Population average in heterogeneous societies



Notes: Initial population: 10^3 agents. Iterations: $5 \times 10^3 t$.
Repetitions: 10. When heterogeneity is forced, decentralized societies (dark) have almost double the population average than the centralized ones (light)



Notes: Initial population: 10^3 agents. Iterations: $5 \times 10^3 t$.
Repetitions: 10. When homogeneity is forced, decentralized societies (dark) have almost double the population average than the centralized ones (light)

Figure 7. Population average in homogeneous societies

4. Conclusions

The bacterial-based approach described in this paper extends agent-based modeling in order to study of complex social dynamics in artificial societies. Inspired by microbial adaptation and conjugation of DNA plasmids, the computational model we have designed simulates how CAS may adapt to dynamic environments.

We have codified motor behavior in strategic genomes that can be shared by owners, reproduced by receivers, mutated and mixed. Finally, we have seen how constraints like centralization or homogeneity reduce global fitness. Based on our results, we can infer that O, R and P absence benefits collective adaptation to dynamic environments. Thus, we can conclude that in a

basic model with scarcity of information, a CAS could achieve its best configuration by increasing decentralization and heterogeneity while keeping the minimum degree of similarity between nodes and the minimum presence of hubs (Barabási and Oltvai, 2004). Therefore, if we focus on adaptability, the increase of these two variables is positive for the system, at least if their context is dynamic or modified by regular changes (i.e. variability of resource location).

We have come to the conclusion that even though both variables impact group adaptation, decentralization has greater influence. In considering social systems as a subset of CAS, even when a society is homogeneous, creative solutions can evolve and improve collective intelligence. However, this development and its impact on group adaptation and global development can only be achieved by means of P2P dynamics without central control. That is, decentralization is the key in systemic adaptation. According to Sawyer (2005), Mitchell (2009) or Heylighen (2004), there is not an analytical framework more convenient than the CAS paradigm to study social systems. The need of a systemic perspective with a focus on the complexity of social systems was already proposed by Hernández-Carrión (2000), appealing to a context of growing globalization.

These simulations of artificial societies are helpful to justify P2P social dynamics as a positive configuration for social development, as presented by Bauwens (2005), or more recently by Gonzalez-Rodriguez and Kostakis (2015). In conclusion, decentralization and heterogeneity can serve as key elements in understanding an upcoming P2P society, a paradigm in which agent adaptation to dynamic environments shall require the aforementioned properties rather than centralization, closeness and homogeneity. In the future, societies with high degrees of decentralization and heterogeneity will be better able to successfully deal with new challenges.

References

- Barabási, A.L. and Oltvai, Z.N. (2004), "Network biology: understanding the cell's functional organization", *Nature Reviews. Genetics*, Vol. 5 No. 1, pp. 101-113. doi: 10.1038/nrg1272.
- Baran, P. (1964), "On distributed communications networks", *IEEE Transactions on Communications*, Vol. 12 No. 1, pp. 1-9. doi: 10.1109/TCOM.1964.1088883.
- Bauwens, M. (2005), "The political economy of peer production. CTheory, 1", available at: www.informatik.uni-leipzig.de/~graebe/Texte/Bauwens-06.pdf (accessed October 2014).
- Cannon, W.B. (1940), "The wisdom of the body", *The Journal of Nervous and Mental Disease*, Vol. 92 No. 2, pp. 262.
- Davison, J. (1999), "Genetic exchange between bacteria in the environment", *Plasmid*, Vol. 42 No. 1, pp. 73-91. doi: 10.1006/plas.1999.1421.
- Duffy, J., Epstein, J.M. and Axtell, R. (1998), "Growing artificial societies: social science from the bottom up", *Southern Economic Journal*, Vol. 64 No. 3, p. 791. doi: 10.2307/1060800.
- Givigi, S.N. and Schwartz, H.M. (2014), "Decentralized strategy selection with learning automata for multiple pursuer-evader games", *Adaptive Behavior*, Vol. 22 No. 4, pp. 221-234. doi: 10.1177/1059712314526261.
- Gonzalez-Rodriguez, D. and Hernandez-Carrion, J.R. (2014), "A bacterial-based algorithm to simulate complex adaptive systems", in del Pobil, A., Chinellato, E., Martinez-Martin, E., Hallam, J., Cervera, E. and Morales, A. (Eds), *From Animals to Animats 13*, Vol. 8575, Springer International Publishing, Castellón, pp. 250-259. doi: 10.1007/978-3-319-08864-8_24.

- Gonzalez-Rodriguez, D. and Kostakis, V. (2015), "Information literacy and peer-to-peer infrastructures: an autopoietic perspective", *Telematics and Informatics*, Vol. 32 No. 1, pp. 586-593. doi: 10.1016/j.tele.2015.01.001.
- Hernández-Carrión, J.R. (2000), "Quo vadis complexity science? Una vision de la complejidad a partir del enfoque sistémico", *Revista Internacional de Sistemas*, Vol. 10 No. 1, pp. 58-67.
- Heylighen, F. (1999), "The growth of structural and functional complexity during evolution", in Heylighen, F., Bollen, J. and Riegler, A. (Eds), *The Evolution of Complexity*, Kluwer Academic, Dordrecht, pp. 17-44.
- Heylighen, F. (2004), "Complexity and information overload in society: why increasing efficiency leads to decreasing control", *Technological Forecasting and Social Change*, No.1, pp.1-44.
- Izquierdo, L.R., Galán, J.M., Santos, J.I. and Olmo, R.D. (2008), "Modelado de sistemas complejos mediante simulación basada en agentes y mediante dinámica de sistemas", *EMPIRIA. Revista de Metodología de Ciencias Sociales*, Vol. 16 No. 1, pp. 85-112.
- Lansing, J.S. (2003), "Complex adaptive systems", *Annual Review of Anthropology*, Vol. 32 No. 1, pp. 183-204. doi: 10.1146/annurev.anthro.32.061002.093440.
- Lytinen, S.L. and Railsback, S.F. (2012), "The evolution of agent-based simulation platforms: a review of NetLogo 5.0 and ReLogo", *Proceedings of the Fourth International Symposium on Agent-Based Modeling and Simulation (21st European Meeting on Cybernetics and Systems Research. EMCSR 2012)*, pp. 1-11.
- Mitchell, M. (1998), *An Introduction to Genetic Algorithms. A Bradford Book*, The MIT Press, London.
- Mitchell, M. (2009), "Complexity: a guided tour", available at: <http://books.google.es/books/about/Complexity.html?id=sSgzHayrDBsC&pgis=1> (accessed October 2014).
- Muller, S.D., Marchetto, J., Airaghi, S. and Kournoutsakos, P. (2002), "Optimization based on bacterial chemotaxis", *IEEE Transactions on Evolutionary Computation*, Vol. 6 No. 1, pp. 16-29. doi: 10.1109/4235.985689.
- Nemiche, M., Pla-López, R. and Cavero, V. (2013), "Un Modelo Teórico Basado en Agentes para Simular la Evolución de los Comportamientos Sociales en un Mundo Artificial", *Revista Internacional de Sistemas*, Vol. 18 No. 1, pp. 19-28.
- NetLogo, N.U. (2009), "NetLogo 4.1 user manual", *Interface*, Vol. 2 No. 1, pp. 1-414. doi: 10.1093/cvr/cvr013.
- Nurzaman, S.G., Matsumoto, Y., Nakamura, Y., Shirai, K. and Ishiguro, H. (2012), "Bacteria-inspired underactuated mobile robot based on a biological fluctuation", *Adaptive Behavior*, Vol. 20 No. 4, pp. 225-236. doi: 10.1177/1059712312445901.
- Pini, G., Brutschy, A., Pinciroli, C., Dorigo, M. and Birattari, M. (2013), "Autonomous task partitioning in robot foraging: an approach based on cost estimation", *Adaptive Behavior*, Vol. 21 No. 2, pp. 118-136. doi: 10.1177/1059712313484771.
- Robertson, D.A. (2005), "Agent-based modeling toolkits NetLogo, RePast, and Swarm", *Academy of Management Learning and Education*, Vol. 4 No. 1, pp. 524-527. doi: 10.5465/AMLE.2005.19086798.
- Sawyer, R.K. (2005), *Social Emergence*, Cambridge University Press, Cambridge p. 276. doi: 10.1017/CBO9780511734892.
- Simon, H.A. (1991), "Bounded rationality and organizational learning", *Organization Science*, Vol. 2 No. 1, pp. 125-134.
- Stonedahl, F. and Duan, R.U.W. (2011), "Raytracing extension", available at: <https://github.com/fstonedahl/RayTracing-Extension> (accessed February 15, 2014).
- Thomas, C.M. and Nielsen, K.M. (2005), "Mechanisms of, and barriers to, horizontal gene transfer between bacteria", *Nature Reviews. Microbiology*, Vol. 3 No. 1, pp. 711-721. doi: 10.1038/nrmicro1234.

About the authors

Diego Gonzalez-Rodriguez is a Computer Systems Engineer, Master in Artificial Intelligence and also a Graduate in International Cooperation for Development. He has worked in several research and development projects in different fields such as DNA and bacterial computing, data mining, artificial intelligence and software as a service. Currently he is a PhD Candidate in Information Science at the University Carlos III of Madrid, where he studies the relationship between complex adaptive systems and P2P social dynamics following an evolutionary approach. He has been a Visiting Researcher at the University of Toronto (Canada) and the University of North Carolina at Greensboro (USA). His professional experience includes some projects as Software Engineer in the private and the third sector, and also as a Researcher in universities such as the Universidad Politécnica de Madrid and the Universidad Rey Juan Carlos. He is also Member of the “Group of Economics and Complexity: Information, Communities and Multidisciplinary Networks” at the University of Valencia. Diego Gonzalez-Rodriguez is the corresponding author and can be contacted at: xmunch@xmunch.com

Dr Jose Rodolfo Hernandez-Carrion is an Associate Professor in the Department of Applied Economics at the University of Valencia UVEG (Spain), holding a PhD in Economics. He has been a Visiting Scholar at the University of Bologna, IRES-ER, and CINECA (Italy), University of Limerick (Ireland); University of California at Berkeley, CESLA and UCLA (Los Angeles), University of North Carolina at Greensboro in the USA; Peking University (Beijing) and a Visiting Professor at North-East Normal University (NENU) in Changchun, China. His main teaching subjects have been political economy or political economics, European Community, Computer Science in Business and Economics; now belonging to a UVEG Consolidated Innovative Teaching Group: GCID 84/2009 at the Faculty of Law. He has conducted research in Italy, USA, China and Spain focus on Spatial and Regional Economics and Environmental issues. He is trying to reach new insights connecting systems theory and complexity with his main topics of research.